Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:31:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238284.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6238284 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238284.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:31:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238284.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,088,119
Mapped reads	2,811,834 / 91.05%
Unmapped reads	276,285 / 8.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,805 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	112,484 / 3.64%
Duplication rate	2.99%
Clipped reads	1,334,034 / 43.2%

2.2. ACGT Content

Number/percentage of A's	51,329,346 / 27.56%
Number/percentage of C's	36,101,821 / 19.38%
Number/percentage of T's	56,601,825 / 30.39%
Number/percentage of G's	42,190,583 / 22.65%
Number/percentage of N's	46,687 / 0.03%
GC Percentage	42.03%

2.3. Coverage

Mean	0.0602

Standard Deviation	0.4636

2.4. Mapping Quality

Mean Mapping Quality	44.88

2.5. Mismatches and indels

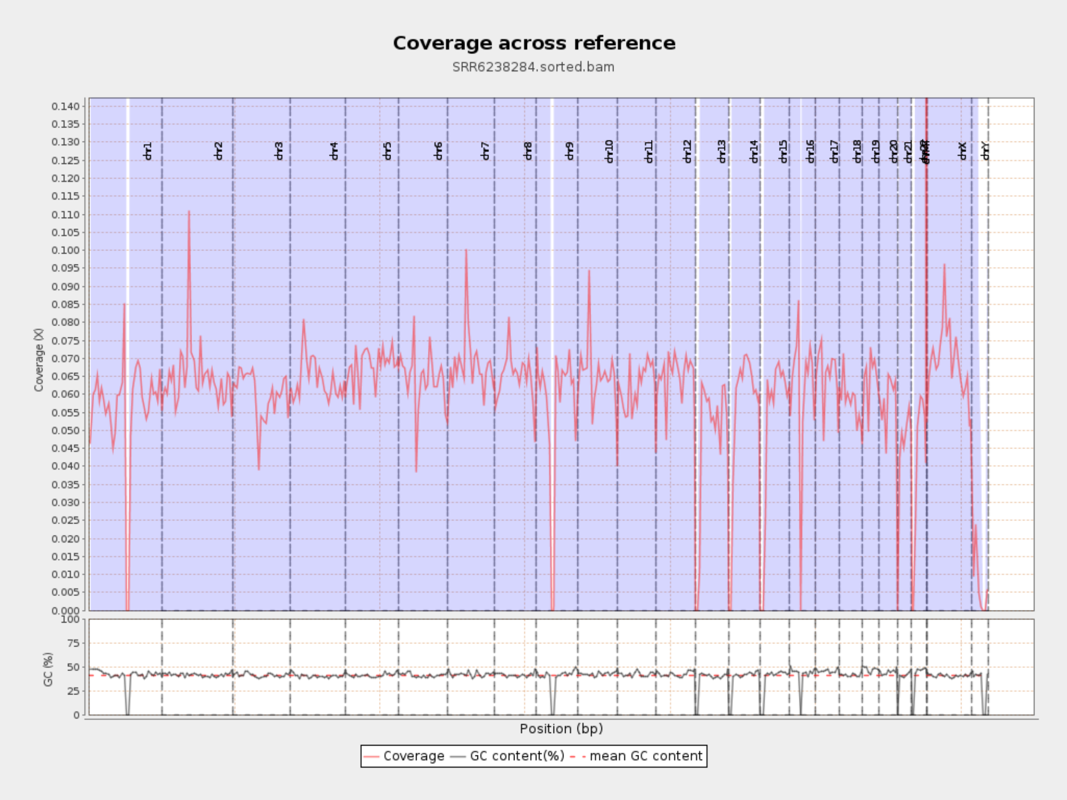
General error rate	0.87%
Mismatches	1,591,426
Insertions	14,884
Mapped reads with at least one insertion	0.52%
Deletions	57,342
Mapped reads with at least one deletion	2.01%
Homopolymer indels	45.33%

2.6. Chromosome stats

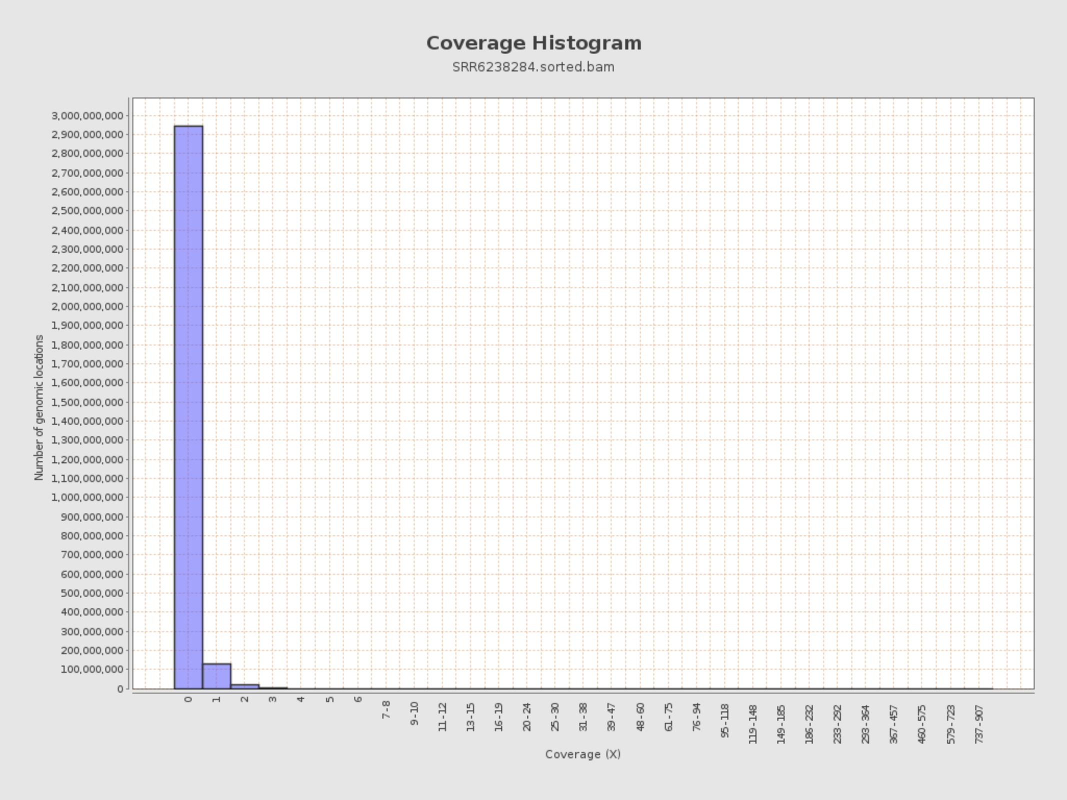
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13920046	0.0558	0.7577
chr2	243199373	15908559	0.0654	0.604
chr3	198022430	11887699	0.06	0.2841
chr4	191154276	12246983	0.0641	0.3162
chr5	180915260	12299201	0.068	0.3044
chr6	171115067	11017001	0.0644	0.3686
chr7	159138663	10941073	0.0688	0.6067

chr8	146364022	9496767	0.0649	0.5616
chr9	141213431	7896261	0.0559	0.4678
chr10	135534747	8947523	0.066	0.4509
chr11	135006516	8370424	0.062	0.4101
chr12	133851895	8739481	0.0653	0.3093
chr13	115169878	5420546	0.0471	0.2528
chr14	107349540	5858907	0.0546	0.3239
chr15	102531392	5250874	0.0512	0.2724
chr16	90354753	5523421	0.0611	0.3331
chr17	81195210	5282896	0.0651	0.3491
chr18	78077248	4567752	0.0585	0.87
chr19	59128983	3778190	0.0639	0.5945
chr20	63025520	3635619	0.0577	0.295
chr21	48129895	2152410	0.0447	0.2844
chr22	51304566	1984675	0.0387	0.2273
chrMT	16571	11691	0.7055	1.0092
chrX	155270560	10738340	0.0692	0.3526
chrY	59373566	488761	0.0082	0.1743

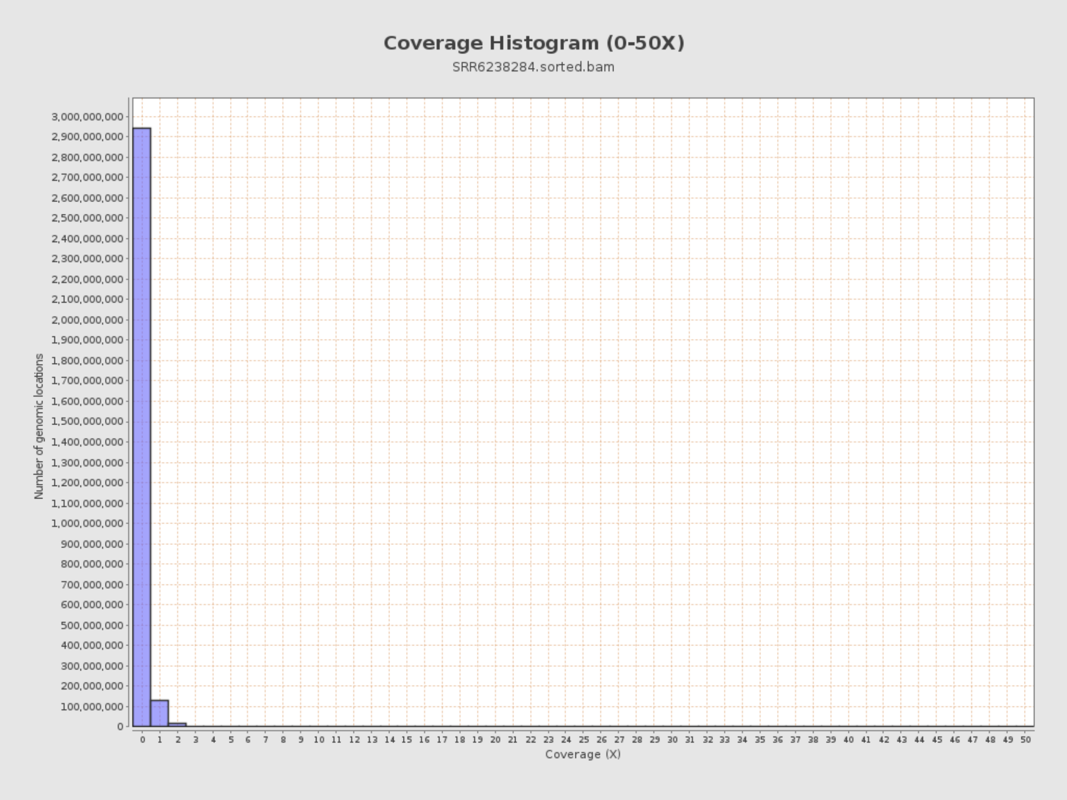
3. Results : Coverage across reference



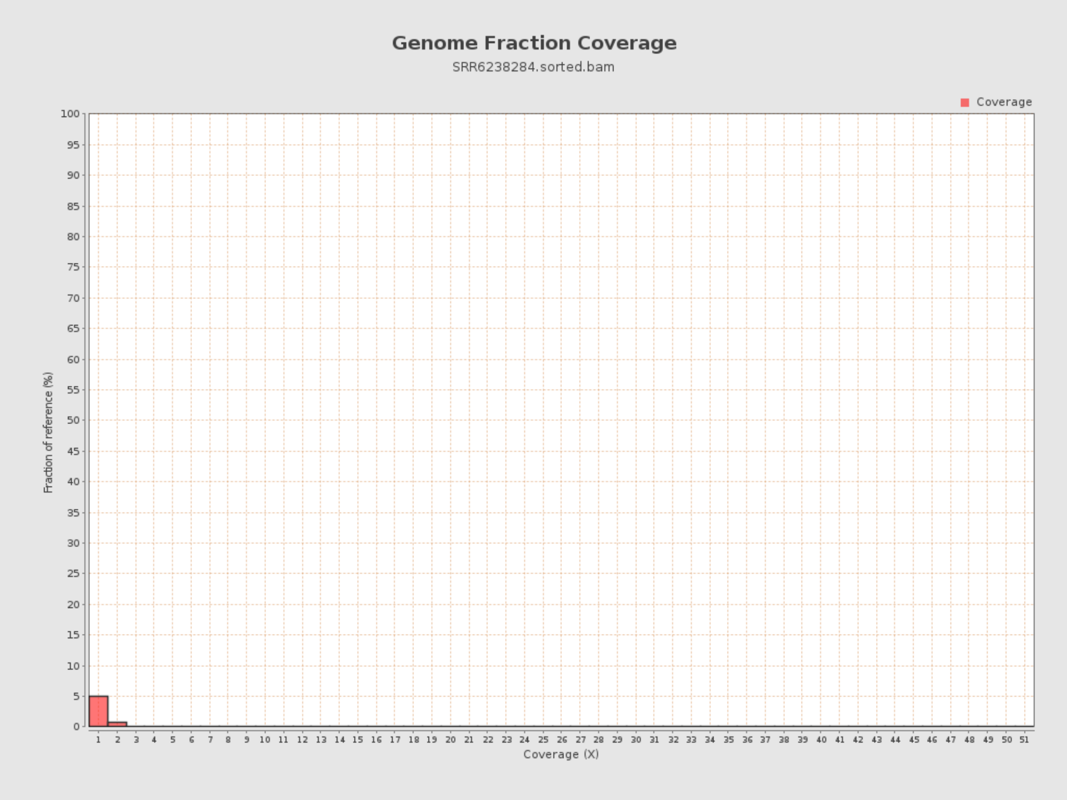
4. Results : Coverage Histogram



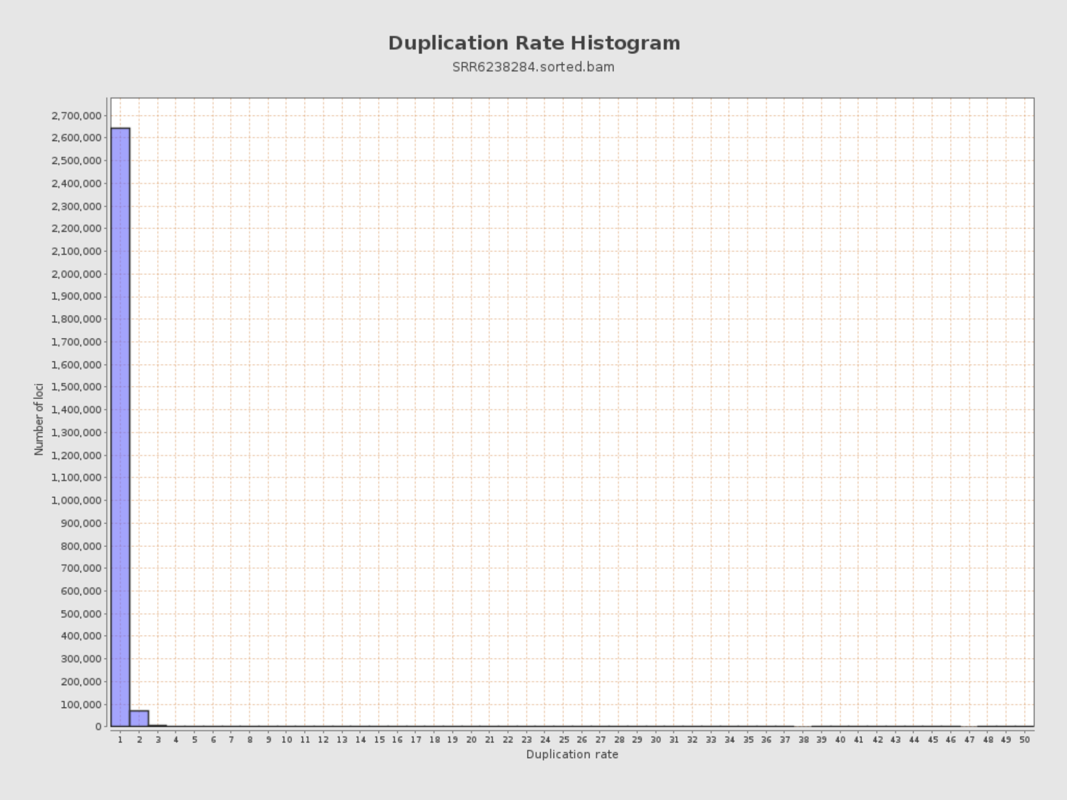
5. Results : Coverage Histogram (0-50X)



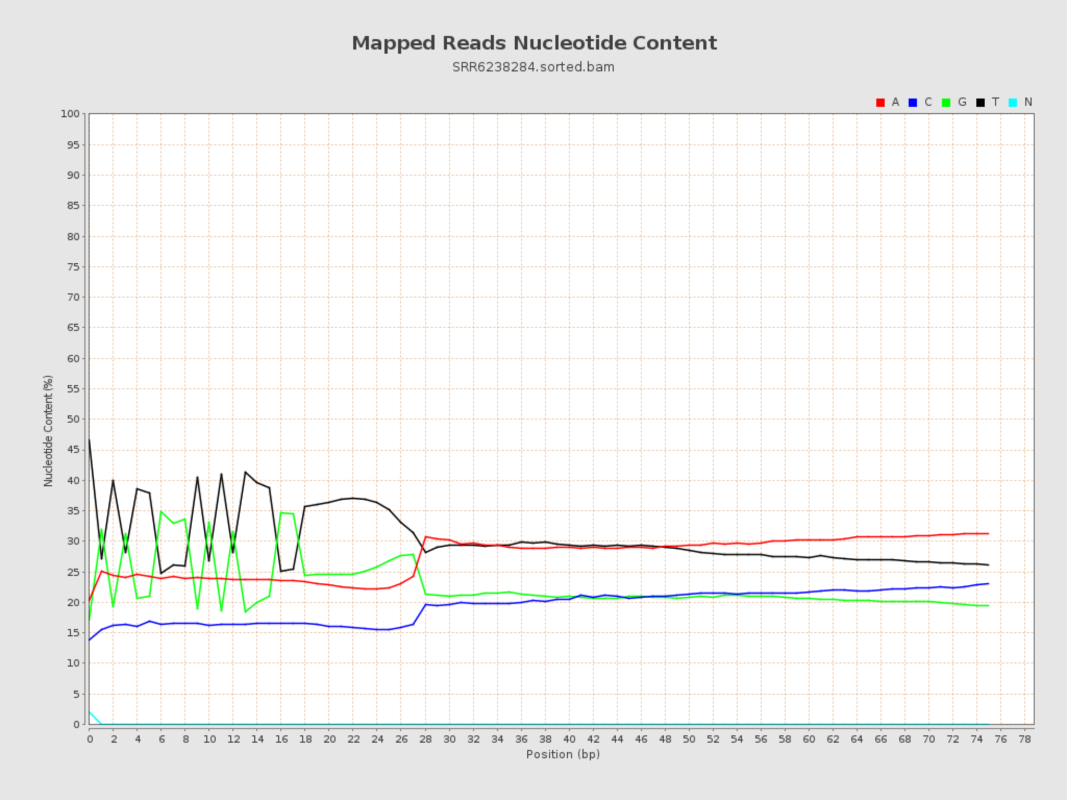
6. Results : Genome Fraction Coverage



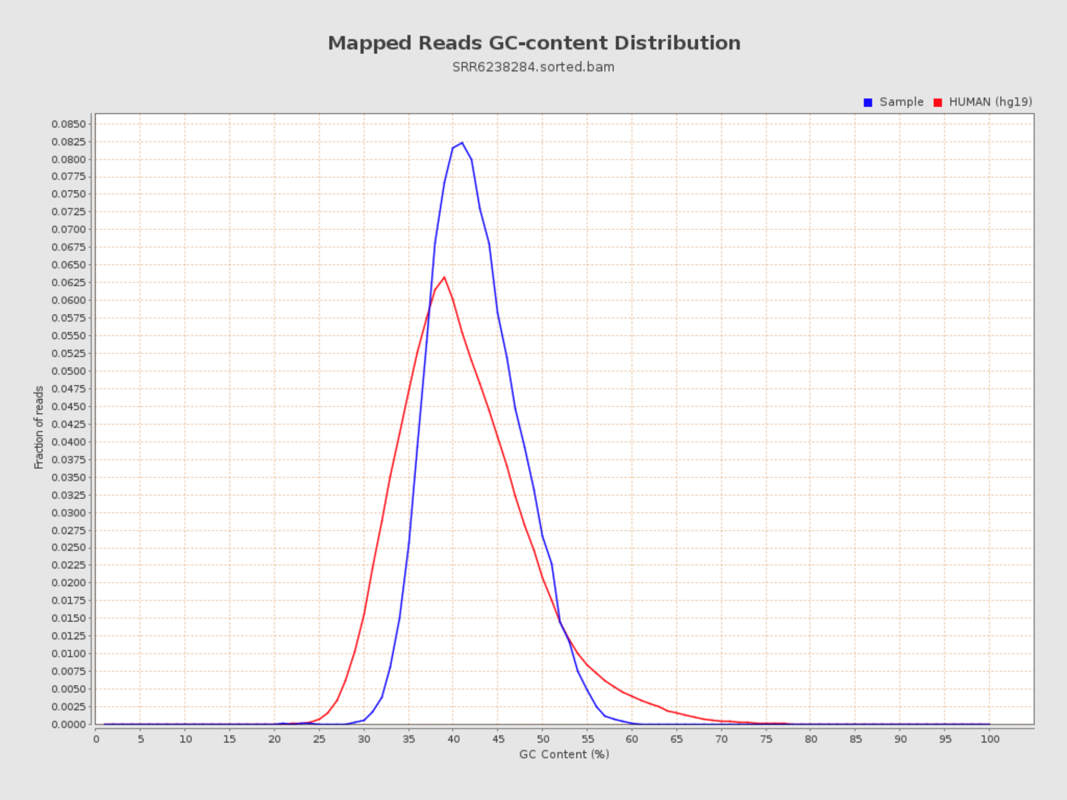
7. Results : Duplication Rate Histogram



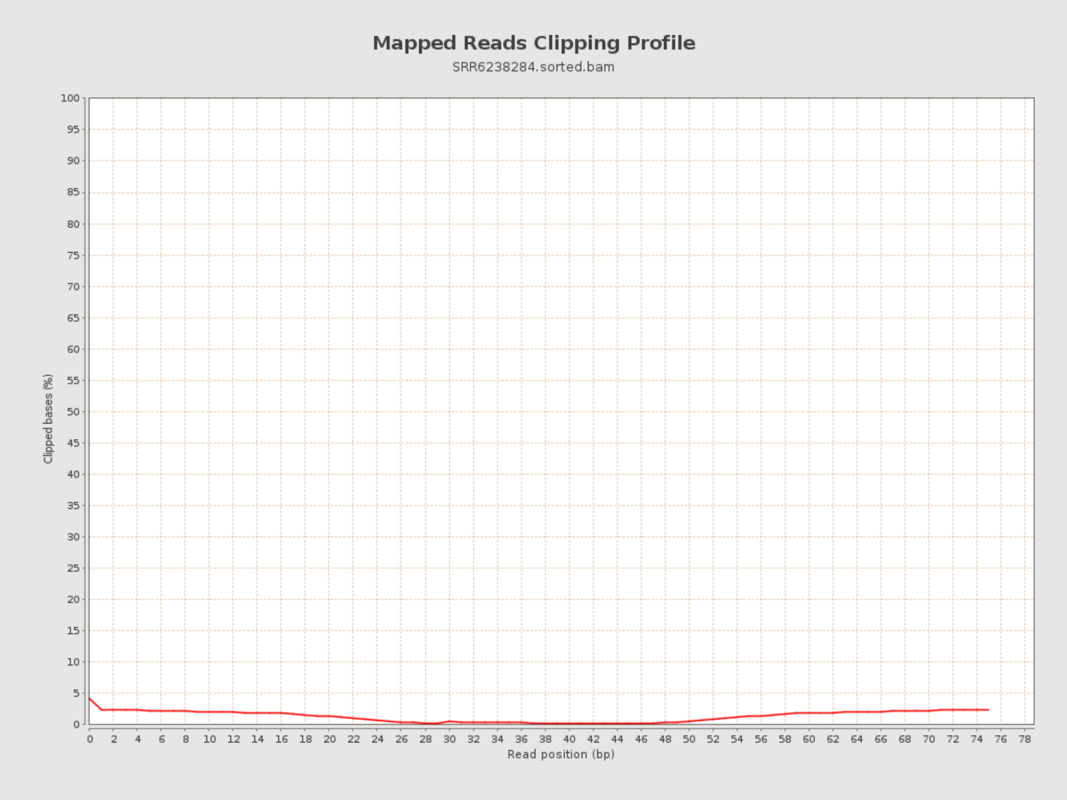
8. Results : Mapped Reads Nucleotide Content



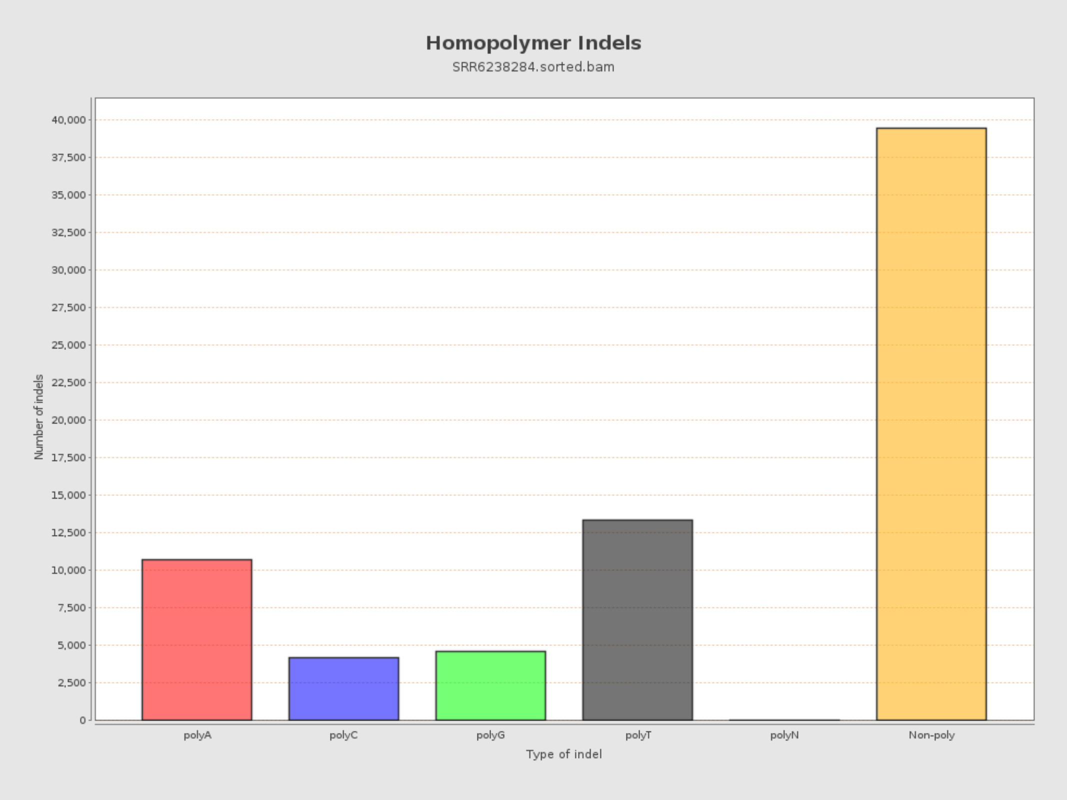
9. Results : Mapped Reads GC-content Distribution



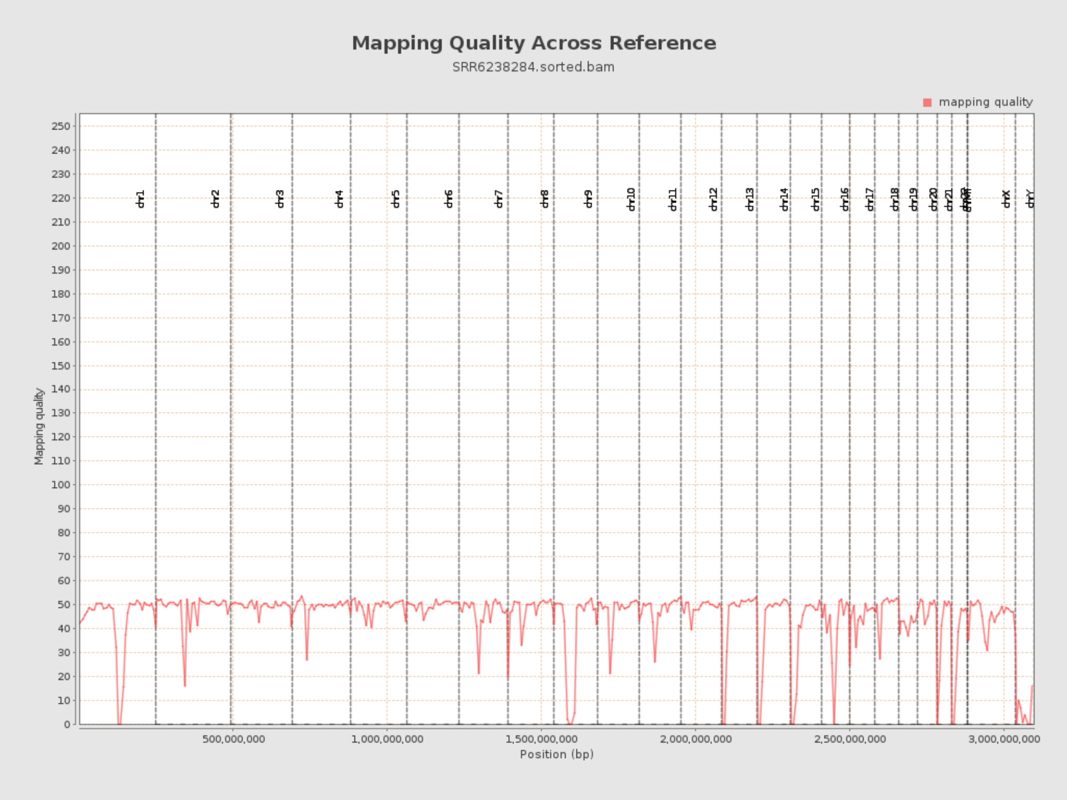
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram